

SEQ Search Summary

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 19:31:23 ; Search time 979 Seconds
(without alignments)
11794.282 Million cell updates/sec

Title: US-09-935-799A-1 *in DNA databases*
Perfect score: 2718
Sequence: 1 aggatggtataaatcatctc.....gctaatacctggtgcccgctg 2718

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2718	100.0	2718	6	ABA95999	DE 10042051 Aba95999 Corynebac
2	2682	98.7	349980	5	AAH68526	EP 1108770 Aah68526 C glutami
3	2423	89.1	2446	8	ACC59461	WD 03/40293 Acc59461 C glutami
4	2416	88.9	2439	4	AAF70990	WD 01/00804 Aaf70990 C. glutam
5	2202	81.0	2202	5	AAH65692	EP Aah65692 C glutami
6	895	32.9	110000	4	AAI99682_34	Continuation (35 o
7	895	32.9	110000	4	AAI99683_34	Continuation (35 o

Applicant's priority doc. →
large fragment →

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 21:35:19 ; Search time 217 Seconds
(without alignments)
6950.952 Million cell updates/sec

Title: US-09-935-799A-1
Perfect score: 2718
Sequence: 1 aggatggtataaatcatctc.....gctaatacctggtgcccgctg 2718

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB	Query		
	1	895	32.9	4403765	3	US-09-103-840A-2		Sequence 2, Appli
	2	895	32.9	4411529	3	US-09-103-840A-1		Sequence 1, Appli
	3	655.8	24.1	2085	4	US-09-252-991A-14016		Sequence 14016, A
	4	655.8	24.1	2115	4	US-09-252-991A-14060		Sequence 14060, A
c	5	655.8	24.1	2397	4	US-09-252-991A-14210		Sequence 14210, A
	6	597	22.0	2118	4	US-09-328-352-331		Sequence 331, App
	7	578.8	21.3	2130	4	US-09-489-039A-6065		Sequence 6065, Ap
	8	522.4	19.2	2169	4	US-09-489-039A-1771		Sequence 1771, Ap
c	9	520.6	19.2	1467	4	US-09-489-039A-5993		Sequence 5993, Ap
c	10	453.6	16.7	1257	4	US-09-489-039A-1557		Sequence 1557, Ap
	11	433.2	15.9	1980	4	US-09-543-681A-1841		Sequence 1841, Ap

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2004, 00:24:39 ; Search time 1130 Seconds
(without alignments)
10915.414 Million cell updates/sec

Title: US-09-935-799A-1
Perfect score: 2718
Sequence: 1 aggatggtataaatcatctc.....gctaatacctggtgcccgcctg 2718

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Nakagawa

Result	%					Query		DB		ID	Description
No.	Score	Match	Length	DB	ID						
1	2718	100.0	2718	9	US-09-935-799A-1						Sequence 1, Appli
2	2718	100.0	2867	9	US-09-935-799A-4						Sequence 4, Appli
3	2682	98.7	3309400	9	US-09-738-626-1						Sequence 1, Appli
4	2202	81.0	2202	9	US-09-738-626-727						Sequence 727, App
5	655.8	24.1	2067	13	US-10-282-122A-30509						Sequence 30509, A
6	638.8	23.5	2064	13	US-10-282-122A-31913						Sequence 31913, A
c 7	609	22.4	609	9	US-09-738-626-728						Sequence 728, App
8	577.8	21.3	1884	13	US-10-282-122A-33754						Sequence 33754, A
9	511.4	18.8	2105	13	US-10-282-122A-19910						Sequence 19910, A
10	507	18.7	2166	13	US-10-282-122A-6643						Sequence 6643, Ap
11	502	18.5	2151	13	US-10-282-122A-40110						Sequence 40110, A
12	498.2	18.3	1750	13	US-10-282-122A-23804						Sequence 23804, A
13	464.8	17.1	2218	9	US-09-881-752A-75						Sequence 75, Appl
14	457	16.8	2148	13	US-10-282-122A-32977						Sequence 32977, A
15	440.2	16.2	1608	13	US-10-335-977-869						Sequence 869, App
16	324.4	11.9	1387	13	US-10-282-122A-36500						Sequence 36500, A
17	234.4	8.6	828	13	US-10-335-977-867						Sequence 867, App
18	234.4	8.6	837	13	US-10-335-977-868						Sequence 868, App
19	197	7.2	201	9	US-09-738-626-729						Sequence 729, App
20	181.2	6.7	1545	9	US-09-974-300-4240						Sequence 4240, Ap
c 21	153.4	5.6	1840	10	US-09-746-660A-1						Sequence 1, Appli
c 22	153.4	5.6	1840	13	US-10-450-055-5						Sequence 5, Appli
23	127.6	4.7	302	9	US-09-956-004-117						Sequence 117, App
24	74.2	2.7	456	9	US-09-974-300-8328						Sequence 8328, Ap
25	74.2	2.7	849	9	US-09-974-300-8316						Sequence 8316, Ap
26	62.2	2.3	243	13	US-10-335-977-866						Sequence 866, App
27	62.2	2.3	246	13	US-10-335-977-865						Sequence 865, App
28	60.4	2.2	198	13	US-10-282-122A-18011						Sequence 18011, A
29	45	1.7	522	13	US-10-335-977-864						Sequence 864, App
30	44.4	1.6	1830121	15	US-10-329-960-1						Sequence 1, Appli
31	44.4	1.6	1830121	16	US-10-329-670-1						Sequence 1, Appli
32	43.8	1.6	1116	13	US-10-282-122A-22229						Sequence 22229, A
33	41.4	1.5	594	13	US-10-142-426-10						Sequence 10, Appl
34	41.4	1.5	594	15	US-10-123-155-10						Sequence 10, Appl
35	41.4	1.5	594	15	US-10-146-731-10						Sequence 10, Appl
36	41.4	1.5	594	15	US-10-140-472-10						Sequence 10, Appl
37	41.4	1.5	594	15	US-10-141-761-10						Sequence 10, Appl
38	41.4	1.5	594	15	US-10-142-885-10						Sequence 10, Appl
39	41.4	1.5	594	15	US-10-158-790-10						Sequence 10, Appl
40	41.4	1.5	594	16	US-10-137-871-10						Sequence 10, Appl
41	41.4	1.5	594	16	US-10-140-923-10						Sequence 10, Appl
42	41.4	1.5	594	16	US-10-141-756-10						Sequence 10, Appl
43	41.4	1.5	594	16	US-10-141-759-10						Sequence 10, Appl
44	41.4	1.5	594	16	US-10-140-805-10						Sequence 10, Appl
45	41.4	1.5	594	16	US-10-140-864-10						Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-935-799A-1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 21:32:27 ; Search time 6163 Seconds
(without alignments)
13169.789 Million cell updates/sec

Title: US-09-935-799A-1
Perfect score: 2718
Sequence: 1 aggatggtataaatcatctc.....gctaatacctggtgcccgctg 2718

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	215.6	7.9	667	12	BJ032628		BJ032628	BJ032628
	2	206.2	7.6	454	28	BZ298052		BZ298052	CG3984.r1
c	3	202	7.4	626	12	BJ622724		BJ622724	BJ622724
c	4	201.4	7.4	617	12	BJ625616		BJ625616	BJ625616
	5	157	5.8	816	13	BQ157960		BQ157960	NF009G12P
	6	145.8	5.4	409	14	D57198		D57198	HUM279C04B
c	7	144	5.3	605	10	BF632543		BF632543	NF028D03D
	8	118.8	4.4	774	28	AQ869689		AQ869689	nbeb0035F
	9	115.4	4.2	1286	28	BZ579625		BZ579625	msh2_688.
	10	111	4.1	931	14	CD074477		CD074477	MA3-0001U
c	11	108.8	4.0	1200	28	BZ551729		BZ551729	pacs1-60_
c	12	108	4.0	1282	28	BZ560788		BZ560788	pacs2-164
	13	102.4	3.8	1047	28	BH770794		BH770794	LLMGtag53
c	14	100.8	3.7	492	10	BE248719		BE248719	NF010F10D
c	15	90.4	3.3	446	28	AQ869690		AQ869690	nbeb0035F
c	16	89.4	3.3	461	28	AQ915452		AQ915452	nbeb0057E
	17	89.2	3.3	675	29	CC820798		CC820798	FECPC1C5 U
c	18	77.4	2.8	204	12	BI698773		BI698773	Th655 The
	19	66.4	2.4	574	28	BZ896338		BZ896338	NaRP8_018
	20	52.4	1.9	885	13	BX425603		BX425603	BX425603
	21	47.2	1.7	1159	29	CNS015XR		AL106041	Drosophil
c	22	46.6	1.7	240	28	BZ893845		BZ893845	HL7_0172
	23	46.2	1.7	712	13	BX416727		BX416727	BX416727
c	24	45.2	1.7	1108	13	BX382084		BX382084	BX382084
	25	45.2	1.7	1201	13	BX356664		BX356664	BX356664
c	26	44.8	1.6	797	29	CNS003F8		AL064634	Drosophil
c	27	44.6	1.6	1065	13	BX380296		BX380296	BX380296
	28	44.6	1.6	1201	13	BX381961		BX381961	BX381961
c	29	43.8	1.6	849	13	BX462111		BX462111	BX462111
	30	43.6	1.6	902	29	CNS006QP		AL065804	Drosophil
c	31	43.6	1.6	1201	13	BX381961		BX381961	BX381961
c	32	42.4	1.6	448	12	BI614427		BI614427	RH43790.5
c	33	42.4	1.6	595	12	BI605424		BI605424	RH71033.5
c	34	42.4	1.6	724	10	BF493806		BF493806	AT02162.5
	35	42.4	1.6	779	10	BF489650		BF489650	AT25758.5
c	36	42.4	1.6	1079	29	AG135323		AG135323	Pan trogl
c	37	42	1.5	995	12	BG474941		BG474941	602490874
c	38	42	1.5	1101	29	CNS00FOO		AL070854	Drosophil
	39	41.6	1.5	420	28	BZ892300		BZ892300	Hm2_0195.
	40	41.6	1.5	762	29	CC483184		CC483184	CH240_311
c	41	41.2	1.5	631	14	CK133167		CK133167	RE17678.3
c	42	41.2	1.5	681	12	BG636062		BG636062	SD13651.5
	43	41	1.5	647	14	CF900631		CF900631	A0317G07-
	44	41	1.5	848	12	BI655284		BI655284	603284087
c	45	41	1.5	922	10	BE285387		BE285387	601091450

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2004, 21:25:40 ; Search time 10147 Seconds
(without alignments)
11609.970 Million cell updates/sec

Title: US-09-935-799A-1
Perfect score: 2718
Sequence: 1 aggatggtataaatcatctc.....gctaatcctggtgcccgctg 2718

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%		Query		DB	ID	Description
Result No.	Score	Match	Length					
1	2718	100.0	2718	6	AX394271		AX394271	Sequence
2	2718	100.0	2867	6	AX394274		AX394274	Sequence
3	2682	98.7	332050	1	AP005276		AP005276	Corynebac
4	2682	98.7	349980	6	AX127145		AX127145	Sequence
5	2423	89.1	2446	6	AX756599		AX756599	Sequence
6	2416	88.9	2439	6	AX066109		AX066109	Sequence
7	2202	81.0	2202	6	AX120811		AX120811	Sequence
8	2202	81.0	2202	6	BD162928		BD162928	Novel pol
9	1222.2	45.0	349895	1	BX248359		BX248359	Corynebac
10	982	36.1	5964	1	AF434799		AF434799	Corynebac
11	895	32.9	14493	1	AE007132		AE007132	Mycobacte
12	895	32.9	348676	15	BX842581		Bx842581	Mycobacte
13	893.4	32.9	318050	1	BX248344		BX248344	Mycobacte
14	661.2	24.3	300774	1	AE016912		AE016912	Chromobac
15	659.8	24.3	215050	1	AL646057		AL646057	Ralstonia
c 16	655.8	24.1	10602	1	AE004874		AE004874	Pseudomon
c 17	638.8	23.5	300933	1	AE016791		AE016791	Pseudomon
18	633.2	23.3	2304	1	AF182514		AF182514	Pseudomon
19	626.4	23.0	11160	1	AE005239		AE005239	Escherich
20	626.4	23.0	262278	1	AP002552		AP002552	Escherich
21	613.8	22.6	10909	1	AE012384		AE012384	Xanthomon
c 22	612.2	22.5	311963	1	AE016872		AE016872	Pseudomon
23	612	22.5	300413	1	AE016757		AE016757	Escherich
c 24	609	22.4	609	6	AX120812		AX120812	Sequence
c 25	609	22.4	609	6	BD162929		BD162929	Novel pol
26	607.6	22.4	12003	1	AE000165		AE000165	Escherich
27	607.6	22.4	136742	1	ECU82598		U82598	Escherichia
c 28	601	22.1	12256	1	AE013810		AE013810	Yersinia
c 29	601	22.1	334050	1	AJ414151		AJ414151	Yersinia
30	598.8	22.0	10924	1	AE011930		AE011930	Xanthomon
31	597	22.0	2118	6	AR317781		AR317781	Sequence
32	596	21.9	10052	1	AE002498		AE002498	Neisseria
33	596	21.9	349980	6	AX044032		AX044032	Sequence

Mockel (Appl.)

WO 02/18597
 "ATCC - GenBank
 EP

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 18, 2004, 15:49:32 ; Search time 4140 Seconds
(without alignments)
5568.503 Million cell updates/sec

Title: US-09-935-799A-2 in DNA databases
Perfect score: 3934
Sequence: 1 MALKRPEEKTIVKIVTIKQTD.....VQAMWDERYPGGAPVSSGGH 772

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

-
Q=/cgn2_1/USPTO_spool_p/US09935799/runat_17052004_115454_3734/app_query.fasta_1.
967

-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09935799_@CGN_1_1_4237_@runat_17052004_115454_3734 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*

```

11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	663.5	16.9	667	12	BJ032628		BJ032628	BJ032628
	2	647.5	16.5	1047	28	BH770794		BH770794	LLMGtag53
	3	565	14.4	454	28	BZ298052		BZ298052	CG3984.r1
c	4	516.5	13.1	617	12	BJ625616		BJ625616	BJ625616
c	5	508	12.9	626	12	BJ622724		BJ622724	BJ622724
	6	461.5	11.7	816	13	BQ157960		BQ157960	NF009G12P
c	7	437	11.1	605	10	BF632543		BF632543	NF028D03D
c	8	427	10.9	1282	28	BZ560788		BZ560788	pacs2-164
	9	403	10.2	1286	28	BZ579625		BZ579625	msh2_688.
	10	376	9.6	409	14	D57198		D57198	HUM279C04B
	11	369	9.4	774	28	AQ869689		AQ869689	nbeb0035F
	12	363	9.2	931	14	CD074477		CD074477	MA3-0001U
c	13	320.5	8.1	461	28	AQ915452		AQ915452	nbeb0057E
c	14	318.5	8.1	446	28	AQ869690		AQ869690	nbeb0035F
c	15	303	7.7	492	10	BE248719		BE248719	NF010F10D
	16	266	6.8	675	29	CC820798		CC820798	FECPC1C5 U
c	17	265	6.7	1200	28	BZ551729		BZ551729	pacs1-60_
	18	242	6.2	574	28	BZ896338		BZ896338	NaRP8_018
c	19	201.5	5.1	204	12	BI698773		BI698773	Th655 The
c	20	187.5	4.8	240	28	BZ893845		BZ893845	HL7_0172
c	21	142.5	3.6	827	9	AJ455413		AJ455413	AJ455413
	22	141	3.6	2833	11	AK044448		AK044448	Mus muscu
	23	139	3.5	3894	11	AK085602		AK085602	Mus muscu
	24	134.5	3.4	3270	29	AY408630		AY408630	Homo sapi
c	25	131.5	3.3	811	9	AJ452083		AJ452083	AJ452083
c	26	130	3.3	1793	10	BF218103		BF218103	601885805
c	27	129	3.3	958	13	BU421186		BU421186	603954658
	28	127.5	3.2	3578	11	AK050819		AK050819	Mus muscu

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 18, 2004, 14:45:36 ; Search time 6807 Seconds
(without alignments)
4915.649 Million cell updates/sec

Title: US-09-935-799A-2
Perfect score: 3934
Sequence: 1 MALKRPEEKTIVKIVTIKQTD.....VQAMWDERYPGGAPVSSGGH 772

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

-
Q=/cgn2_1/USPTO_spool_p/US09935799/runat_17052004_115453_3722/app_query.fasta_1.
967

-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09935799@CGN_1_1_5265@runat_17052004_115453_3722 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*

11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*
 15: em_ba:*
 16: em_fun:*
 17: em_hum:*
 18: em_in:*
 19: em_mu:*
 20: em_om:*
 21: em_or:*
 22: em_ov:*
 23: em_pat:*
 24: em_ph:*
 25: em_pl:*
 26: em_ro:*
 27: em_sts:*
 28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	No.	Score	Match Length	DB	ID	
	1	3930	99.9	2439	6	AX066109 WO 01/00804
	2	3930	99.9	2446	6	AX756599 WO 03/40293
	3	3930	99.9	2718	6	AX394271 WO 02/18597
	4	3930	99.9	2867	6	AX394274 "
	5	3930	99.9	332050	1	AP005276 GenBank
	6	3930	99.9	349980	6	AX127145 EP
	7	3742	95.1	2202	6	AX120811 EP
	8	3742	95.1	2202	6	BD162928
	9	2932.5	74.5	349895	1	BX248359
	10	2421.5	61.6	348676	15	BX842581
	11	2414.5	61.4	14493	1	AE007132
	12	2407.5	61.2	318050	1	BX248344
	13	1891.5	48.1	300774	1	AE016912
c	14	1872.5	47.6	276034	1	AE017015
c	15	1867.5	47.5	264504	1	AE017041
	16	1855.5	47.2	2118	6	AR317781

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 18, 2004, 13:54:06 ; Search time 683 Seconds
(without alignments)
4801.770 Million cell updates/sec

Title: US-09-935-799A-2
Perfect score: 3934
Sequence: 1 MALKRPEEKTIVKIVTIKQTD.....VQAMWDERYPGGAPVSSGGH 772

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

-
Q=/cgn2_1/USPTO_spool_p/US09935799/runat_17052004_115453_3714/app_query.fasta_1.
967

-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09935799_@CGN_1_1_708_@runat_17052004_115453_3714 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	3930	99.9	2439	4	AAF70990	Wo 01/00804 Aaf70990 C. glutam
	2	3930	99.9	2446	8	ACC59461	Wo 03/40293 Acc59461 C glutami
	3	3930	99.9	2718	6	ABA95999	DE Aba95999 Corynebac
	4	3930	99.9	349980	5	AAH68526	EP Aah68526 C glutami
	5	3742	95.1	2202	5	AAH65692	Aah65692 C glutami
	6	2421.5	61.6	110000	4	AAI99682_34	Continuation (35 o
	7	2414.5	61.4	110000	4	AAI99683_34	Continuation (35 o
	8	2133.5	54.2	34088	4	AAS59566	Aas59566 Propionib
	9	2133.5	54.2	34088	7	ACF64495	Acf64495 Propionib
	10	1855.5	47.2	2118	8	ADA29044	Ada29044 DNA encod
	11	1849	47.0	2067	7	ACA42639	Aca42639 Prokaryot
c	12	1849	47.0	349980	6	ABQ81846	Abq81846 Bifidobac
	13	1844.5	46.9	110000	6	ABA90521_04	Continuation (5 of
	14	1811	46.0	2064	7	ACA44043	Aca44043 Prokaryot
	15	1805	45.9	2119	7	ACC70208	Acc70208 Nucleotid
c	16	1795.5	45.6	11658	3	AAA81506	Aaa81506 N. mening
	17	1794.5	45.6	110000	3	AAA81489_0	Aaa81489 N. mening
	18	1794.5	45.6	110000	3	AAA81489_1	Continuation (2 of
	19	1794.5	45.6	349980	3	AAF21610	Aaf21610 Neisseria
	20	1794.5	45.6	349980	3	AAF21611	Aaf21611 Neisseria
	21	1785.5	45.4	2079	7	ABZ40793	Abz40793 N. gonorr
	22	1727	43.9	1884	7	ACA45884	Aca45884 Prokaryot
c	23	1718	43.7	2172	6	ABQ90088	Abq90088 M. capsul
	24	1686.5	42.9	2151	7	ACA52240	Aca52240 Prokaryot
	25	1681	42.7	2148	7	ACA45107	Aca45107 Prokaryot
	26	1676	42.6	2166	7	ACA18773	Aca18773 Prokaryot
	27	1664.5	42.3	2105	7	ACA32040	Aca32040 Prokaryot
	28	1627	41.4	2218	2	AAX13957	Aax13957 H. pylori
	29	1561.5	39.7	1750	7	ACA35934	Aca35934 Prokaryot
c	30	1137	28.9	110000	7	ACF67367_39	Continuation (40 o
	31	1137	28.9	110000	7	ACF65388_09	Continuation (10 o
	32	1130	28.7	1803	7	ACF70813	Acf70813 Photorhab
	33	1109.5	28.2	1387	7	ACA48630	Aca48630 Prokaryot
c	34	1047	26.6	609	5	AAH65693	Aah65693 C glutami
	35	917	23.3	1545	6	ABK76949	Abk76949 Bacillus
	36	802	20.4	3019	5	AAS89033	Aas89033 DNA encod
	37	798	20.3	702	6	ABN21506	Abn21506 Human ORF
	38	786	20.0	2635	5	AAS89235	Aas89235 DNA encod
c	39	786	20.0	3209	5	AAS93121	Aas93121 DNA encod
	40	716	18.2	2109	5	AAS88654	Aas88654 DNA encod
c	41	676.5	17.2	349980	5	AAH41226	Aah41226 Pyrococcu
c	42	676.5	17.2	349980	5	AAH41225	Aah41225 Pyrococcu
	43	662	16.8	2235	5	AAS89030	Aas89030 DNA encod
c	44	542.5	13.8	733	6	ABQ18409	Abq18409 Oligonucl
	45	542.5	13.8	733	6	ABQ18408	Abq18408 Oligonucl

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 18, 2004, 16:06:22 ; Search time 154 Seconds
(without alignments)
2781.962 Million cell updates/sec

Title: US-09-935-799A-2
Perfect score: 3934
Sequence: 1 MALKRPEEKT VKIVTIKQTD.....VQAMWDERYPGGAPVSSGGH 772

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

-Q=/cgn2_1/USPTO_spool_p/US09935799/runat_17052004_115454_3750/app_query.fasta_1.967

-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09935799_@CGN_1_1_85_@runat_17052004_115454_3750 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					Description
	No.	Score	Match	Length	ID	
	1	2421.5	61.6	4411529	3	US-09-103-840A-1
	2	2414.5	61.4	4403765	3	US-09-103-840A-2
	3	1855.5	47.2	2118	4	US-09-328-352-331
	4	1849	47.0	2085	4	US-09-252-991A-14016
	5	1849	47.0	2115	4	US-09-252-991A-14060
c	6	1849	47.0	2397	4	US-09-252-991A-14210
	7	1803	45.8	2130	4	US-09-489-039A-6065
	8	1679.5	42.7	2169	4	US-09-489-039A-1771
	9	1575	40.0	1980	4	US-09-543-681A-1841
c	10	1523	38.7	1467	4	US-09-489-039A-5993
c	11	1199.5	30.5	1257	4	US-09-489-039A-1557
c	12	585.5	14.9	747	4	US-09-252-991A-14123
	13	386	9.8	1830121	4	US-09-557-884-1
	14	386	9.8	1830121	4	US-09-643-990A-1
	15	343.5	8.7	1593	4	US-09-540-236-563
c	16	343.5	8.7	89047	4	US-09-596-002-34
	17	276	7.0	302	4	US-08-976-259-117
	18	191.5	4.9	1308	4	US-09-252-991A-1179
	19	170.5	4.3	1995	4	US-09-328-352-2930
	20	168	4.3	1050	4	US-09-252-991A-1269
c	21	166.5	4.2	4403765	3	US-09-103-840A-2
c	22	165	4.2	1428	4	US-09-252-991A-14802
	23	165	4.2	1668	4	US-09-252-991A-14950
c	24	162.5	4.1	4411529	3	US-09-103-840A-1
	25	156	4.0	24417	2	US-08-846-762-1
c	26	154.5	3.9	1905	4	US-09-252-991A-7829
	27	153.5	3.9	1389	4	US-09-543-681A-1118
	28	152.5	3.9	1392	4	US-09-252-991A-7744
	29	152.5	3.9	1491	4	US-09-489-039A-1601
	30	152	3.9	8654	4	US-08-961-527-98
c	31	149	3.8	640681	4	US-09-790-988-1
	32	147.5	3.7	1602	4	US-09-107-532A-2352
	33	146.5	3.7	1443	4	US-09-489-039A-5874
c	34	146	3.7	3395	4	US-08-956-171E-119
c	35	146	3.7	36138	4	US-08-311-731A-136
	36	144.5	3.7	3687	4	US-09-252-991A-1193
	37	144.5	3.7	4266	4	US-09-252-991A-1234
c	38	144	3.7	11679	4	US-09-328-352-1377
	39	143.5	3.6	1758	4	US-09-328-352-2007
	40	142.5	3.6	1566	4	US-09-134-001C-1453
	41	140.5	3.6	1422	4	US-09-489-039A-7028
c	42	140.5	3.6	41171	4	US-08-311-731A-122
	43	140	3.6	89047	4	US-09-596-002-34
	44	139	3.5	1278	4	US-09-489-039A-1038
c	45	139	3.5	1398	4	US-09-489-039A-3060

ALIGNMENTS

RESULT 1
US-09-103-840A-1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 18, 2004, 16:39:45 ; Search time 781 Seconds
(without alignments)
4485.754 Million cell updates/sec

Title: US-09-935-799A-2
Perfect score: 3934
Sequence: 1 MALKRPEEKTIVKIVTIKQTD.....VQAMWDERYPGGAPVSSGGH 772

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

-Q=/cgn2_1/USPTO_spool_p/US09935799/runat_17052004_115455_3836/app_query.fasta_1.967

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09935799_@CGN_1_1_333_@runat_17052004_115455_3836
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	3930	99.9		2718	9	US-09-935-799A-1	Sequence 1, Appli
2	3930	99.9		2867	9	US-09-935-799A-4	Sequence 4, Appli
3	3930	99.9	3309400		9	US-09-738-626-1	Sequence 1, Appli
4	3742	95.1		2202	9	US-09-738-626-727	Sequence 727, App
5	1849	47.0		2067	13	US-10-282-122A-30509	Sequence 30509, A
6	1811	46.0		2064	13	US-10-282-122A-31913	Sequence 31913, A
7	1727	43.9		1884	13	US-10-282-122A-33754	Sequence 33754, A
8	1686.5	42.9		2151	13	US-10-282-122A-40110	Sequence 40110, A
9	1681	42.7		2148	13	US-10-282-122A-32977	Sequence 32977, A
10	1676	42.6		2166	13	US-10-282-122A-6643	Sequence 6643, Ap
11	1664.5	42.3		2105	13	US-10-282-122A-19910	Sequence 19910, A
12	1627	41.4		2218	9	US-09-881-752A-75	Sequence 75, Appl
13	1561.5	39.7		1750	13	US-10-282-122A-23804	Sequence 23804, A
14	1452	36.9		1608	13	US-10-335-977-869	Sequence 869, App
15	1109.5	28.2		1387	13	US-10-282-122A-36500	Sequence 36500, A
c 16	1047	26.6		609	9	US-09-738-626-728	Sequence 728, App
17	917	23.3		1545	9	US-09-974-300-4240	Sequence 4240, Ap
18	775	19.7		828	13	US-10-335-977-867	Sequence 867, App
19	775	19.7		837	13	US-10-335-977-868	Sequence 868, App
20	386	9.8	1830121		15	US-10-329-960-1	Sequence 1, Appli
21	386	9.8	1830121		16	US-10-329-670-1	Sequence 1, Appli
c 22	343.5	8.7	89047		13	US-10-672-787-34	Sequence 34, Appl
23	338	8.6	1116		13	US-10-282-122A-22229	Sequence 22229, A
24	332.5	8.5	849		9	US-09-974-300-8316	Sequence 8316, Ap
25	276	7.0	302		9	US-09-956-004-117	Sequence 117, App
26	240	6.1	456		9	US-09-974-300-8328	Sequence 8328, Ap
27	184	4.7	2559		15	US-10-156-761-4174	Sequence 4174, Ap
28	184	4.7	9025608		15	US-10-156-761-1	Sequence 1, Appli
29	183	4.7	1167		13	US-10-389-647-211	Sequence 211, App
30	179.5	4.6	522		13	US-10-335-977-864	Sequence 864, App
31	175	4.4	243		13	US-10-335-977-866	Sequence 866, App
32	175	4.4	246		13	US-10-335-977-865	Sequence 865, App
c 33	174	4.4	9025608		15	US-10-156-761-1	Sequence 1, Appli
c 34	163.5	4.2	3309400		9	US-09-738-626-1	Sequence 1, Appli
35	161.5	4.1	1602		15	US-10-156-761-4524	Sequence 4524, Ap
36	161.5	4.1	1930		13	US-10-282-122A-8621	Sequence 8621, Ap
c 37	160	4.1	7693		13	US-10-072-012-133	Sequence 133, App
38	159.5	4.1	1467		15	US-10-156-761-5569	Sequence 5569, Ap

Nakagawa